

SEQUENCE LISTING

<110> Benkovic, Stephen J

<120> Treatment of Bacterial Induced Diseases Using DNA Methyl Transferase Inhibitors

<130> 00-387-P

<140> To be Assigned

<141> Herewith

<150> US 09/996,420

<151> 2001-11-29

<150> US 09/578,991

<151> 2000-05-25

<150> US 60/174,256

<151> 2000-01-03

<150> US 60/154,582

<151> 1999-09-17

<150> US 60/135,870

<151> 1999-05-25

<150> US 09/269,137

<151> 1999-03-16

<150> US 60/020,089

<151> 1996-09-19

<160> 24

<170> PatentIn version 3.2

<210> 1

<211> 1698

<212> DNA

<213> Rhizobium meliloti

<220>

<221> CDS

<222> (304)..(1431)

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gcgggcagca ttttgcgcg tgcgggatcg ccgatcaacg agccgatcaag agctatgtcc 120

gggccttcct tcataacttcg atgataatcg aagtatcgcg gacgggcaag accccggatcg 180

gcggcgcctg gacgatgact cctgcggcga cgcaaatttt tccggcgcct tcaggcttg 240

gtaaccatct tcggtaacca taagcctatc gtcactccga ctaagcgtat ttgcgagttg 300

cca atg tca tca gtt gtt tcg ctt gcc gaa atc tcc cgt gcc gcc cgt			348
Met Ser Ser Val Val Ser Leu Ala Glu Ile Ser Arg Ala Ala Arg			
1 5 10 15			
ccg ctg aac tgg ctg gac agc atc atc aag gga gat tgc gtg gcc gcg			396
Pro Leu Asn Trp Leu Asp Ser Ile Ile Lys Gly Asp Cys Val Ala Ala			
20 25 30			
ctg aac gcg ctt ccc gat cat tcg gtc gat gtc gtc ttc gcc gac ccg			444
Leu Asn Ala Leu Pro Asp His Ser Val Asp Val Val Phe Ala Asp Pro			
35 40 45			
ccc tat aat ctt cag ctc ggc ggc acg ttg cac cgg ccc gat cag tcg			492
Pro Tyr Asn Leu Gln Leu Gly Gly Thr Leu His Arg Pro Asp Gln Ser			
50 55 60			
ctg gtc gat gca gtg gac gac gat tgg gac cag ttt gct tcc ttc gaa			540
Leu Val Asp Ala Val Asp Asp Trp Asp Gln Phe Ala Ser Phe Glu			
65 70 75			
gcc tat gac gct ttc acc cgc gcc tgg ctg ctt gcc tgc cgg cgt gtc			588
Ala Tyr Asp Ala Phe Thr Arg Ala Trp Leu Leu Ala Cys Arg Arg Val			
80 85 90 95			
ctg aag ccc acc ggc acg ctc tgg gtc atc ggt tcc tac cac aat atc			636
Leu Lys Pro Thr Gly Thr Leu Trp Val Ile Gly Ser Tyr His Asn Ile			
100 105 110			
ttc cgg gtc ggc gcg atc ctc cag gac ctg cac ttc tgg gtc ttg aac			684
Phe Arg Val Gly Ala Ile Leu Gln Asp Leu His Phe Trp Val Leu Asn			
115 120 125			
gat atc atc tgg cgc aag acc caa ccc gat gcc gaa ctt caa ggg cgc			732
Asp Ile Ile Trp Arg Lys Thr Gln Pro Asp Ala Glu Leu Gln Gly Arg			
130 135 140			
cgc ttc cag aac gcg cat gaa acg ctg atc tgg gcg acg gcg aac gcc			780
Arg Phe Gln Asn Ala His Glu Thr Leu Ile Trp Ala Thr Ala Asn Ala			
145 150 155			
aag gcc aag ggt tat acc ttc aac tac gaa gcg atg aag gcg gcg aac			828
Lys Ala Lys Gly Tyr Thr Phe Asn Tyr Glu Ala Met Lys Ala Ala Asn			
160 165 170 175			
gac gac gtt cag atg cgc tcc gac tgg ctg ttc ccc atc tgc tcc ggt			876
Asp Asp Val Gln Met Arg Ser Asp Trp Leu Phe Pro Ile Cys Ser Gly			
180 185 190			
tcc gag cgg ctg aag ggc gac gac ggc aag aaa gta cac ccg acg caa			924
Ser Glu Arg Leu Lys Gly Asp Asp Gly Lys Lys Val His Pro Thr Gln			
195 200 205			
aag ccg gaa gcg ctg ctt gcc cgc atc ctg atg gcc tcg acc aag ccc			972
Lys Pro Glu Ala Leu Leu Ala Arg Ile Leu Met Ala Ser Thr Lys Pro			
210 215 220			

ggg gac gtc gtg ctt gat ccg ttc ttc ggc tcc ggc acc acc ggg gcg Gly Asp Val Val Leu Asp Pro Phe Phe Gly Ser Gly Thr Thr Gly Ala 225 230 235	1020
gtc gcc aag cgc ctc ggc cg ^g cac ttc gtc ggg atc gag cgc gag cag Val Ala Lys Arg Leu Gly Arg His Phe Val Gly Ile Glu Arg Glu Gln 240 245 250 255	1068
gac tat atc gat gcc gcc gaa cgt atc g ^c gc ^g gtc gag cc ^g ctc Asp Tyr Ile Asp Ala Ala Glu Arg Ile Ala Ala Val Glu Pro Leu 260 265 270	1116
ggc aag gcc acg ctc tcg gtc atg acc ggc aag aag g ^c g ^g gag cc ^g cgc Gly Lys Ala Thr Leu Ser Val Met Thr Gly Lys Lys Ala Glu Pro Arg 275 280 285	1164
gtc gcc ttc aac act ctg gtg gaa agc ggg ctc atc aag ccc ggc acg Val Ala Phe Asn Thr Leu Val Glu Ser Gly Leu Ile Lys Pro Gly Thr 290 295 300	1212
gtt ctg acg gat g ^c g ^g aag cgc cgc tac agc g ^c g ^g atc gtc cgc gcc gac Val Leu Thr Asp Ala Lys Arg Arg Tyr Ser Ala Ile Val Arg Ala Asp 305 310 315	1260
ggc acg ctg g ^c g ^g tcc ggc ggc gag gct gga tcc att cac cgc ctc ggc Gly Thr Leu Ala Ser Gly Gly Glu Ala Gly Ser Ile His Arg Leu Gly 320 325 330 335	1308
gca aaa gtg cag ggc ctc gac gcc tgc aac ggc tgg acc ttc tgg cac Ala Lys Val Gln Gly Leu Asp Ala Cys Asn Gly Trp Thr Phe Trp His 340 345 350	1356
t ^t c gag gag gga agc gta ttg aaa ccg atc gac gag ctc aga tcc gtc Phe Glu Glu Gly Ser Val Leu Lys Pro Ile Asp Glu Leu Arg Ser Val 355 360 365	1404
att cga aac gac ctg gca aaa ctg aac tgatcaacca cttccgcctg Ile Arg Asn Asp Leu Ala Lys Leu Asn 370 375	1451
ggtcttcgat aggccccc ttccggttt t ^t tgcc ^t ttca gtccggatg agcgcttaa	1511
acgcccgaat ccgaagagga ttccggggct ttgtatcaat gccccggatc agcgtagag	1571
catggcagcc gctgccagga gggtgcccg tccgaagctg gataccgtag ccgcgagatc	1631
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tcgacat	1698

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<211> 376
<212> PRT
<213> Rhizobium meliloti

<400> 2

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1 5 10 15

Leu Asn Trp Leu Asp Ser Ile Ile Lys Gly Asp Cys Val Ala Ala Leu
20 25 30

Asn Ala Leu Pro Asp His Ser Val Asp Val Val Phe Ala Asp Pro Pro
35 40 45

Tyr Asn Leu Gln Leu Gly Gly Thr Leu His Arg Pro Asp Gln Ser Leu
50 55 60

Val Asp Ala Val Asp Asp Asp Trp Asp Gln Phe Ala Ser Phe Glu Ala
65 70 75 80

Tyr Asp Ala Phe Thr Arg Ala Trp Leu Leu Ala Cys Arg Arg Val Leu
85 90 95

Lys Pro Thr Gly Thr Leu Trp Val Ile Gly Ser Tyr His Asn Ile Phe
100 105 110

Arg Val Gly Ala Ile Leu Gln Asp Leu His Phe Trp Val Leu Asn Asp
115 120 125

Ile Ile Trp Arg Lys Thr Gln Pro Asp Ala Glu Leu Gln Gly Arg Arg
130 135 140

Phe Gln Asn Ala His Glu Thr Leu Ile Trp Ala Thr Ala Asn Ala Lys
145 150 155 160

Ala Lys Gly Tyr Thr Phe Asn Tyr Glu Ala Met Lys Ala Ala Asn Asp
165 170 175

Asp Val Gln Met Arg Ser Asp Trp Leu Phe Pro Ile Cys Ser Gly Ser
180 185 190

Glu Arg Leu Lys Gly Asp Asp Gly Lys Lys Val His Pro Thr Gln Lys
195 200 205

Pro Glu Ala Leu Leu Ala Arg Ile Leu Met Ala Ser Thr Lys Pro Gly
210 215 220

Asp Val Val Leu Asp Pro Phe Phe Gly Ser Gly Thr Thr Gly Ala Val		
225	230	235
Ala Lys Arg Leu Gly Arg His Phe Val Gly Ile Glu Arg Glu Gln Asp		
245	250	255
Tyr Ile Asp Ala Ala Ala Glu Arg Ile Ala Ala Val Glu Pro Leu Gly		
260	265	270
Lys Ala Thr Leu Ser Val Met Thr Gly Lys Lys Ala Glu Pro Arg Val		
275	280	285
Ala Phe Asn Thr Leu Val Glu Ser Gly Leu Ile Lys Pro Gly Thr Val		
290	295	300
Leu Thr Asp Ala Lys Arg Arg Tyr Ser Ala Ile Val Arg Ala Asp Gly		
305	310	315
Thr Leu Ala Ser Gly Gly Glu Ala Gly Ser Ile His Arg Leu Gly Ala		
325	330	335
Lys Val Gln Gly Leu Asp Ala Cys Asn Gly Trp Thr Phe Trp His Phe		
340	345	350
Glu Glu Gly Ser Val Leu Lys Pro Ile Asp Glu Leu Arg Ser Val Ile		
355	360	365
Arg Asn Asp Leu Ala Lys Leu Asn		
370	375	

<210> 3
<211> 1731
<212> DNA
<213> Brucella abortus

<220>
<221> CDS
<222> (394) .. (1524)

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caaaactacac ccgacaggca cttcactctg cgagcggctg ccacacacac tgcatcatcg 120
tcatttgccg ccggatcata gacaaaaga aataaccaag ctttattgtat tgcgacatat 180

gccgttccag ccttcacat ggatcacgatgcgtcacatgcataattatctcg	240
ccttattggc cgccaaagg ccgcaaagcc gggcttccc tgttatattt agaaaagatt	300
taggatttca agcacttggc gttaagcgca tatttaccct aggcagtaac cataggaaca	360
agtttttgc gttcacaggt aatcgagtat ccc atg tcc cta gta cgt ctt gcg Met Ser Leu Val Arg Leu Ala	414
1 5	
cat gag ttg ccc atc gag gcc ccg cgt acc gcc tgg ctc gac tcc atc His Glu Leu Pro Ile Glu Ala Pro Arg Thr Ala Trp Leu Asp Ser Ile	462
10 15 20	
atc aaa ggt gat tgc gtt tcc gcg ctg gag cgc ctg ccg gat cat tcc Ile Lys Gly Asp Cys Val Ser Ala Leu Glu Arg Leu Pro Asp His Ser	510
25 30 35	
gta gac gtc atc ttt gcc gat ccg ccc tat aat ctc cag ctt ggc ggc Val Asp Val Ile Phe Ala Asp Pro Pro Tyr Asn Leu Gln Leu Gly Gly	558
40 45 50 55	
gat ctg cac cgt ccg gat cag tcc atg gtc agc gcc gtc gac gat cat Asp Leu His Arg Pro Asp Gln Ser Met Val Ser Ala Val Asp Asp His	606
60 65 70	
tgg gac cag ttt gaa agc ttc cag gcc tat gac gcc ttc acc ccg gcc Trp Asp Gln Phe Glu Ser Phe Gln Ala Tyr Asp Ala Phe Thr Arg Ala	654
75 80 85	
tgg ctg ctc gcc tgc cgc cgt gtc ctg aag ccg aat ggc acc atc tgg Trp Leu Ala Cys Arg Arg Val Leu Lys Pro Asn Gly Thr Ile Trp	702
90 95 100	
gtc atc ggt tcc tat cac aat att ttc ccg gtc ggc acg cag ttg cag Val Ile Gly Ser Tyr His Asn Ile Phe Arg Val Gly Thr Gln Leu Gln	750
105 110 115	
gat ctg ggc ttc tgg ctc ctc aac gac att gtc tgg cgc aag acc aat Asp Leu Gly Phe Trp Leu Leu Asn Asp Ile Val Trp Arg Lys Thr Asn	798
120 125 130 135	
ccc atg ccg aat ttc cgt ggc ccg cgt ttc cag aat ggc cat gaa acg Pro Met Pro Asn Phe Arg Gly Arg Arg Phe Gln Asn Ala His Glu Thr	846
140 145 150	
ctg atc tgg gct tcg cgt gag cag aag ggc aag gga tat act ttc aat Leu Ile Trp Ala Ser Arg Glu Gln Lys Gly Lys Gly Tyr Thr Phe Asn	894
155 160 165	
tac gag ggc atg aaa gcg gcc aat gac gat gtc cag atg cgt tcg gac Tyr Glu Gly Met Lys Ala Ala Asn Asp Asp Val Gln Met Arg Ser Asp	942
170 175 180	
tgg ctg ttc ccg atc tgc acc ggc agt gaa cgc ctg aag gac gag aac Trp Leu Phe Pro Ile Cys Thr Gly Ser Glu Arg Leu Lys Asp Glu Asn	990
185 190 195	

ggc gac aag gtc cac ccg acc cag aag ccg gaa gca ctt ctc gcg cgc Gly Asp Lys Val His Pro Thr Gln Lys Pro Glu Ala Leu Leu Ala Arg 200 205 210 215	1038
atc atg atg gct tca agc aag ccg ggc gac gtt att ctc gac cca ttc Ile Met Met Ala Ser Ser Lys Pro Gly Asp Val Ile Leu Asp Pro Phe 220 225 230	1086
ttc ggt tcc ggc acg acc ggc gcg gtc gcc aag cgg ctt ggc cgc cat Phe Gly Ser Gly Thr Thr Gly Ala Val Ala Lys Arg Leu Gly Arg His 235 240 245	1134
ttc gtc ggc atc gag cgt gaa cag ccc tat atc gac gcc gca acc gcc Phe Val Gly Ile Glu Arg Glu Gln Pro Tyr Ile Asp Ala Ala Thr Ala 250 255 260	1182
cgc atc aat gcc gtg gag ccg ctt ggc aag gcg gaa ctc acg gtg atg Arg Ile Asn Ala Val Glu Pro Leu Gly Lys Ala Glu Leu Thr Val Met 265 270 275	1230
acc ggc aag cgc gca gag ccg cgc gtg gcc ttc acg acg gta atg gaa Thr Gly Lys Arg Ala Glu Pro Arg Val Ala Phe Thr Ser Val Met Glu 280 285 290 295	1278
gcg ggc ctt ttg cgt ccg gga acc gtg ctt tgt gat gaa cgc cgc cgt Ala Gly Leu Leu Arg Pro Gly Thr Val Leu Cys Asp Glu Arg Arg Arg 300 305 310	1326
ttt gcc gcc att gtt cgc gcc gat ggg acg ctg acg gcc aac ggc gaa Phe Ala Ala Ile Val Arg Ala Asp Gly Thr Leu Thr Ala Asn Gly Glu 315 320 325	1374
gcc ggt tca atc cat cgt att ggc gcc agg gtt caa ggg ttc gat gcc Ala Gly Ser Ile His Arg Ile Gly Ala Arg Val Gln Gly Phe Asp Ala 330 335 340	1422
tgc aat ggc tgg acc ttc tgg cac ttt gag gaa aac ggc gta ctg aag Cys Asn Gly Trp Thr Phe Trp His Phe Glu Glu Asn Gly Val Leu Lys 345 350 355	1470
cct atc gat gcc ctg cgc aag atc atc cgc gaa cag atg gct gcg gca Pro Ile Asp Ala Leu Arg Lys Ile Ile Arg Glu Gln Met Ala Ala Ala 360 365 370 375	1518
ggc gca taagaaaactt taatatcgga cgatctccag taaactctga tagcaaggcg Gly Ala	1574
ctcgaagttt tcaaacttcg ggcccttca ttcttcaga aagaaaagctg tcgcggccgc aaatcgctcg ccagtttggc tgccgtggta aaatgcacccg cctgccagcc cgcttgcttc gcacaccttcca cattgtgcat cgtgtcatcg atgaaga	1634 1694 1731

<211> 377

<212> PRT

<213> Brucella abortus

<400> 4

Met Ser Leu Val Arg Leu Ala His Glu Leu Pro Ile Glu Ala Pro Arg
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Thr Ala Trp Leu Asp Ser Ile Ile Lys Gly Asp Cys Val Ser Ala Leu
20 25 30

Glu Arg Leu Pro Asp His Ser Val Asp Val Ile Phe Ala Asp Pro Pro
35 40 45

Tyr Asn Leu Gln Leu Gly Gly Asp Leu His Arg Pro Asp Gln Ser Met
50 55 60

Val Ser Ala Val Asp Asp His Trp Asp Gln Phe Glu Ser Phe Gln Ala
65 70 75 80

Tyr Asp Ala Phe Thr Arg Ala Trp Leu Leu Ala Cys Arg Arg Val Leu
85 90 95

Lys Pro Asn Gly Thr Ile Trp Val Ile Gly Ser Tyr His Asn Ile Phe
100 105 110

Arg Val Gly Thr Gln Leu Gln Asp Leu Gly Phe Trp Leu Leu Asn Asp
115 120 125

Ile Val Trp Arg Lys Thr Asn Pro Met Pro Asn Phe Arg Gly Arg Arg
130 135 140

Phe Gln Asn Ala His Glu Thr Leu Ile Trp Ala Ser Arg Glu Gln Lys
145 150 155 160

Gly Lys Gly Tyr Thr Phe Asn Tyr Glu Gly Met Lys Ala Ala Asn Asp
165 170 175

Asp Val Gln Met Arg Ser Asp Trp Leu Phe Pro Ile Cys Thr Gly Ser
180 185 190

Glu Arg Leu Lys Asp Glu Asn Gly Asp Lys Val His Pro Thr Gln Lys
195 200 205

Pro Glu Ala Leu Leu Ala Arg Ile Met Met Ala Ser Ser Lys Pro Gly
210 215 220

Asp Val Ile Leu Asp Pro Phe Phe Gly Ser Gly Thr Thr Gly Ala Val
225 230 235 240

Ala Lys Arg Leu Gly Arg His Phe Val Gly Ile Glu Arg Glu Gln Pro
245 250 255

Tyr Ile Asp Ala Ala Thr Ala Arg Ile Asn Ala Val Glu Pro Leu Gly
260 265 270

Lys Ala Glu Leu Thr Val Met Thr Gly Lys Arg Ala Glu Pro Arg Val
275 280 285

Ala Phe Thr Ser Val Met Glu Ala Gly Leu Leu Arg Pro Gly Thr Val
290 295 300

Leu Cys Asp Glu Arg Arg Phe Ala Ala Ile Val Arg Ala Asp Gly
305 310 315 320

Thr Leu Thr Ala Asn Gly Glu Ala Gly Ser Ile His Arg Ile Gly Ala
325 330 335

Arg Val Gln Gly Phe Asp Ala Cys Asn Gly Trp Thr Phe Trp His Phe
340 345 350

Glu Glu Asn Gly Val Leu Lys Pro Ile Asp Ala Leu Arg Lys Ile Ile
355 360 365

Arg Glu Gln Met Ala Ala Ala Gly Ala
370 375

<210> 5
<211> 255
<212> DNA
<213> Agrobacterium tumefaciens

<220>
<221> CDS
<222> (1)..(255)

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cgg ccc gat cag tcg ctg gtc gat gcc gtt gat gac gaa tgg gac cag				96
Arg Pro Asp Gln Ser Leu Val Asp Ala Val Asp Asp Glu Trp Asp Gln				
20	25	30		
tcc gcc tcc ttc gac gcc tat gac gcc ttc acc cgc gcc tgg ctg ctc				144
Phe Ala Ser Phe Asp Ala Tyr Asp Ala Phe Thr Arg Ala Trp Leu Leu				
35	40	45		
gcc tgc cgc cgt gtg ctg aaa ccg aac ggc acc atc tgg gtc atc ggc				192
Ala Cys Arg Arg Val Leu Lys Pro Asn Gly Thr Ile Trp Val Ile Gly				
50	55	60		
tcc tat cac aat atc ttc cgc gtc ggc gcc atg ctc cag aac ctc gat				240
Ser Tyr His Asn Ile Phe Arg Val Gly Ala Met Leu Gln Asn Leu Asp				
65	70	75	80	
ttc tgg atc ctc aac				255
Phe Trp Ile Leu Asn				
85				

<210> 6
<211> 85
<212> PRT
<213> Agrobacterium tumefaciens

<400> 6

Ile Phe Ala Asp Pro Pro Tyr Asn Leu Gln Leu Gly Gly Asn Val His				
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Arg Pro Asp Gln Ser Leu Val Asp Ala Val Asp Asp Glu Trp Asp Gln				
20	25	30		

Phe Ala Ser Phe Asp Ala Tyr Asp Ala Phe Thr Arg Ala Trp Leu Leu				
35	40	45		

Ala Cys Arg Arg Val Leu Lys Pro Asn Gly Thr Ile Trp Val Ile Gly				
50	55	60		

Ser Tyr His Asn Ile Phe Arg Val Gly Ala Met Leu Gln Asn Leu Asp				
65	70	75	80	

Phe Trp Ile Leu Asn				
85				

<210> 7
<211> 2093

<212> DNA

<213> Helicobacter pylori

<220>

<221> CDS

<222> (202)..(1278)

<400> 7

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tcgtttaaaa taggtgggaa taggttagctt ctatcatttg atgcatttga tgagaacaaa 120

gctaggact aaacattaag atagccttaa aacgcttgc ttaaaatggc cagagtagca 180

gatataaaag gctagttaat c atg gat ttt tta aaa gaa aac tta aac act 231
Met Asp Phe Leu Lys Glu Asn Leu Asn Thr
1 5 10

atc ata gag ggg gat tgt tta gaa aaa ttg aaa gat ttt cct aat aaa 279
Ile Ile Glu Gly Asp Cys Leu Glu Lys Leu Lys Asp Phe Pro Asn Lys
15 20 25

agc gtt gat ttt atc ttt gct gac ccc cca tat ttt atg caa aca gag 327
Ser Val Asp Phe Ile Phe Ala Asp Pro Pro Tyr Phe Met Gln Thr Glu
30 35 40

gga gaa ttg aag cgt ttt gaa ggc aca aaa ttt caa ggc gtt gag gat 375
Gly Glu Leu Lys Arg Phe Glu Gly Thr Lys Phe Gln Gly Val Glu Asp
45 50 55

cat tgg gat aaa ttt ggc tct ttt gaa gaa tac gat acc ttt tgt ttg 423
His Trp Asp Lys Phe Gly Ser Phe Glu Glu Tyr Asp Thr Phe Cys Leu
60 65 70

ggt tgg tta aaa gaa tgc caa agg att tta aaa gat aat ggc act att 471
Gly Trp Leu Lys Glu Cys Gln Arg Ile Leu Lys Asp Asn Gly Thr Ile
75 80 85 90

tgt gtg ata ggg act ttt caa aat att ttt aga att ggt ttt cat ttg 519
Cys Val Ile Gly Thr Phe Gln Asn Ile Phe Arg Ile Gly Phe His Leu
95 100 105

caa aat tta ggg ttt tgg ata ctc aat gat att gtt tgg tac aag agc 567
Gln Asn Leu Gly Phe Trp Ile Leu Asn Asp Ile Val Trp Tyr Lys Ser
110 115 120

aat ccg gtg cct aat ttt gct ggc aag aga cta tgc aac gcc cat gaa 615
Asn Pro Val Pro Asn Phe Ala Gly Lys Arg Leu Cys Asn Ala His Glu
125 130 135

acg ctt att tgg tgc gct aaa cac aaa aac aac aaa gtt acc ttt aat 663
Thr Leu Ile Trp Cys Ala Lys His Lys Asn Asn Lys Val Thr Phe Asn
140 145 150

tat aaa aca atg aag tac ctc aat aac aat aaa caa gaa aaa tcg gtt 711
Tyr Lys Thr Met Lys Tyr Leu Asn Asn Lys Gln Glu Lys Ser Val

ttattacaat aaggataaaag	aaaaaaggga atcttagaa	ttagatcagt ttgctaaaaa	1588
agataacaca tattatTTA	tagaacaAAA aatgcgagat	gaccatgaca gcaccaaaaa	1648
· gagagggcaa atagataact	ttgaaaggaa attagaggct	ttatccatc gttatggcga	1708
aaacattcaa ggctatTTT	atTTtataga tgagggTTG	aataaaaatc aaaattacta	1768
taaagaagaa ttgcaaaaat	tatctgttga ttatggcgtg	cctttgagtt tgtgttatgg	1828
taaggggTTG	tttgaatCTC ttaatatccc	gcaagTTGG gatgaggTTT taagccattt	1888
agtgcgatgg cgtgaaacct	tagccgattt agccagTTG	aatTTTgatg aaaatcTTT	1948
agaaaagTTT agagaaatca	aagatTTAGC gccaagcgtt	tatAGGAAGC ttttgataa	2008
tgatgaaatt ttcaatTTG	tgttaatTTT attcccagaa	caaaaagTTT taaaatgtt	2068
agttagagcat tttagacaac	aaaat		2093

<210> 8
 <211> 359
 <212> PRT
 <213> Helicobacter pylori

<400> 8

Met Asp Phe Leu Lys Glu Asn Leu Asn Thr Ile Ile Glu Gly Asp Cys			
1	5	10	15

Leu Glu Lys Leu Lys Asp Phe Pro Asn Lys Ser Val Asp Phe Ile Phe			
20	25	30	

Ala Asp Pro Pro Tyr Phe Met Gln Thr Glu Gly Glu Leu Lys Arg Phe			
35	40	45	

Glu Gly Thr Lys Phe Gln Gly Val Glu Asp His Trp Asp Lys Phe Gly			
50	55	60	

Ser Phe Glu Glu Tyr Asp Thr Phe Cys Leu Gly Trp Leu Lys Glu Cys			
65	70	75	80

Gln Arg Ile Leu Lys Asp Asn Gly Thr Ile Cys Val Ile Gly Thr Phe			
85	90	95	

Gln Asn Ile Phe Arg Ile Gly Phe His Leu Gln Asn Leu Gly Phe Trp			
100	105	110	

Ile Leu Asn Asp Ile Val Trp Tyr Lys Ser Asn Pro Val Pro Asn Phe
115 120 125

Ala Gly Lys Arg Leu Cys Asn Ala His Glu Thr Leu Ile Trp Cys Ala
130 135 140

Lys His Lys Asn Asn Lys Val Thr Phe Asn Tyr Lys Thr Met Lys Tyr
145 150 155 160

Leu Asn Asn Asn Lys Gln Glu Lys Ser Val Trp Gln Ile Pro Ile Cys
165 170 175

Met Gly Asn Glu Arg Leu Lys Asp Ala Gln Gly Lys Lys Val His Ser
180 185 190

Thr Gln Lys Pro Glu Ala Leu Leu Lys Lys Ile Ile Leu Ser Ala Thr
195 200 205

Lys Pro Lys Asp Ile Ile Leu Asp Pro Phe Phe Gly Thr Gly Thr Thr
210 215 220

Gly Ala Val Ala Lys Ser Met Asn Arg Tyr Phe Ile Gly Ile Glu Lys
225 230 235 240

Asp Ser Phe Tyr Ile Lys Glu Ala Ala Lys Arg Leu Asn Ser Thr Arg
245 250 255

Asp Lys Ser Asp Phe Ile Thr Asn Leu Asp Leu Glu Thr Lys Pro Pro
260 265 270

Lys Ile Pro Met Ser Leu Leu Ile Ser Lys Gln Leu Leu Lys Ile Gly
275 280 285

Asp Phe Leu Tyr Ser Ser Asn Lys Glu Lys Ile Cys Gln Val Leu Glu
290 295 300

Asn Gly Gln Val Arg Asp Asn Glu Asn Tyr Glu Thr Ser Ile His Lys
305 310 315 320

Met Ser Ala Lys Tyr Leu Asn Lys Thr Asn His Asn Gly Trp Lys Phe
325 330 335

Phe Tyr Ala Tyr Tyr Gln Asn Gln Phe Leu Leu Leu Asp Glu Leu Arg

340

345

350

Tyr Ile Cys Gln Arg Asp Ser
355

<210> 9
<211> 20
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Forward primer (IFADDPPY)

<400> 9
atytttygcgbg ayccbccbta 20

<210> 10
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Reverse primer 1 (LDPFFG)

<400> 10
ccraaraaavg grtcsag 17

<210> 11
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: Reverse primer 2 (IGIERE)

<400> 11
tcvcgytcra tvccrat 17

<210> 12
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 12
actcgcgagt caacaga 17

<210> 13
<211> 23

<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 13
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23

<210> 14
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: oligonucleotide

<400> 14
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23

<210> 15
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<213> Artificial

<220>
<223> Description of Artificial Sequence: oligonucleotide

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30

<210> 16
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<212> DNA
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<220>
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<220>
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<222> (11)...(11)
<223> m2a

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23

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<220>
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<223> m2a

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<220>
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45

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<220>
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51

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<220>
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<400> 20
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45

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<212> DNA
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<220>
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<210> 22
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<212> DNA
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<220>
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<210> 23
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<212> DNA
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<220>
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<400> 23
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agagga                                         66

<210> 24
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<212> DNA
<213> Artificial

<220>
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<223> m2a

<220>
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<223> m2a

<400> 24
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